AMENDMENTS

Please amend the claims as follows:

1. (currently amended) A method for obtaining a transgenic maize plant containing a coding sequence of interest (i) that is free of ancillary selection marker sequence comprising:

(a) contacting a maize plant or a cell of a maize plant that lacks an active Ac element transposase, with a transformation vector comprising:

(1) a first expression cassette comprising a coding sequence of interest (i) that is not operably linked to mobilizable sequences of a maize active Ac element transposon; and

(2) a second expression cassette comprising a nucleotide sequence encoding an ancillary selection marker (ii) that is operably linked to the mobilizable sequences of a maize active Ac element transposon, wherein said nucleotide sequence encoding [[a]] the ancillary selection marker (ii) is operably linked to a plant expression control sequence,

to obtain primary transformants;

(b) growing the primary transformants under selective conditions to obtain at least one transformed parental maize plant or maize plant cell having the ancillary selection marker coding sequence (ii);

(c) crossing the selected transformed parental maize plant with a second parental maize plant, said second maize plant having within its genome a sequence encoding an endogenous active Ac element transposase that operates on the mobilizable sequences

of the second expression cassette, wherein said sequence encoding the endogenous active transposase encodes the active Ac element within the R-nj chromosomal locus (an R-nj::AC allele) such that excision of the said Ac element results in the production of anthocyanin-containing sectors on the crown of the seed, including the embryo ~~interrupts expression of a sequence encoding a phenotypic marker for excision (iii)~~, such that an F1 generation is obtained;

(d) selecting a maize plant or cell from the F1 generation having the endogenous active Ac element transposase excised from the sequence encoding a phenotypic marker for excision based on expression of the phenotypic marker for excision ~~expression~~ to identify maize plants containing the coding sequence of interest (i) but lacking the ancillary selection marker coding sequence (ii); and

(e) regenerating a maize plant from the plant or cell selected in (d),

such that a transgenic maize plant containing a coding sequence of interest (i) that is free of foreign ancillary selection marker sequence is produced.

2. (previously presented) The method of claim 1, wherein the selection marker coding sequence (ii) is selected from the group consisting of an antibiotic resistance coding sequence, a herbicide resistance coding sequence, and a phenotypic marker coding sequence.

3. (previously presented) The method of claim 1, wherein the selection marker coding sequence (ii) is selected from the group consisting of an nptII coding sequence and a bar coding sequence.

4. (previously presented) The method of claim 1, wherein the second expression cassette further comprises a nucleotide sequence encoding a reporter protein, wherein the reporter protein is nondestructively detectable.

5. (previously presented) The method of claim 4, wherein the reporter protein is a green fluorescent protein.

6. (canceled)

7. (previously presented) The method of claim 1, wherein the progeny maize plants or cells in step (d) are selected from the group consisting of F1 maize plants, F2 maize plants, and calluses.

8. (canceled)

9. (previously presented) The method of claim 1, wherein the transgenic maize plant belongs to the A188 line.

10. (canceled)

11. (currently amended) The method of claim 1 [[10]], wherein said line is selected from the group consisting of A188 and W22 lines made homozygous for said R-nj::Ac allele.

12. (previously presented) The method of claim 1, wherein the selection of the progeny maize plant or cells in step (d) comprises:

selecting variegated F1 seeds;

selecting F1 maize plants displaying somatic excision of the selection marker coding sequence (ii);

selecting F1 maize plants displaying germinal excision of the selection marker coding sequence (ii);

obtaining F2 maize plant sowing based on these selected F1 plants.

13. (previously presented) The method of claim 1, wherein the selection of the progeny plant or cells in step (d) comprises:

producing calluses from immature F1 embryos,

visually selecting the calluses containing the T-DNA and the selection marker (ii),

multiplying calluses and selecting sectors of excision of the selection marker coding sequence (ii),

regenerating F1 maize plants from the selected sectors of excision.

14. (previously presented) The method as claimed in claim 13, wherein regenerating maize plants from the progeny maize plants or cells selected in (d) comprises culturing selected calluses of immature embryos of F1 ears under conditions that allow regeneration of maize plants.

15-21. (canceled)